

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/563,073
Source: IFWP
Date Processed by STIC: 1/13/06

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/563,073

DATE: 01/13/2006
TIME: 10:27:40

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\01132006\J563073.raw

3 <110> APPLICANT: DOI, Hirofumi
 4 SAITO, Ken
 6 <120> TITLE OF INVENTION: Method of treating diabetes by inhibiting degradation of at
 least one of
 7 CREBL1, ATF6, and HNF-4 alpha by HtrA
 9 <130> FILE REFERENCE: 3190-089
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/563,073
 C--> 12 <141> CURRENT FILING DATE: 2005-12-29
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/014377
 15 <151> PRIOR FILING DATE: 2004-09-30
 17 <150> PRIOR APPLICATION NUMBER: JP P2003-342587
 18 <151> PRIOR FILING DATE: 2003-09-30
 20 <160> NUMBER OF SEQ ID NOS: 35
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1377
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <223> OTHER INFORMATION: DNA that codes for HtrA2 precursor protein
 34 <400> SEQUENCE: 1
 35 atggctgcgc cgagggcggg gcgggggtgca ggctggagcc ttccggcatg gcgggctttg 60
 37 gggggcattc gctgggggag gagaccccgt ttgacccttg acctccggc cctgctgacg 120
 39 tcaggaactt ctgaccccccgg gggccgagtg acttatggga ccccccagtct ctggggcccg 180
 41 ttgtctgttgg gggtaactga acccccggac tgcctgacgt ctgggacccc gggtccccgg 240
 43 gcacaactga ctgcggtgac cccagatacc aggacccggg aggcctcaga gaactctgg 300
 45 acccgttcgc ggcgcgtggct ggcgggtggcg ctggggcgtg gggggggcagt gctgttgtt 360
 47 ttgtggggcg ggggtcgggg tcctccggcc gtcctcgccg ccgtccctag cccggccggcc 420
 49 gcttctcccc ggagtcaactgta caacttcatc gcagatgtgg tggagaagac agcacctgccc 480
 51 gtggctata tcgagatcct ggaccggcac ctttcttgg gccgcgaggt ccctatctcg 540
 53 aacggctcag gattcgtggt ggctgcccgt gggctcatttgc tcaaccaacgc ccatgtgg 600
 55 gctgatcggc gcagagtccg tggagactg ctaagcggcg acacgtatga ggcgtggc 660
 57 acagctgtgg atcccggtgc agacatcgca acgctgagga ttcagactaa ggacgccttc 720
 59 cccacgctgc ctctgggacg ctcagctgtatgc tgcggcaag gggagtttg tggccatg 780
 61 ggaagtccct ttgcactgca gaaacacgatc acatccggca ttgttagctc tgctcagcgt 840
 63 ccagccagag acctgggact ccccaaacc aatgtggaaat acattcaaacc tgatgcagct 900
 65 attgatttttgg gaaactctgg aggtcccttg gttaacctgg atggggaggt gattggagtg 960
 67 aacaccatga aggtcacacgc tggaaatctcc ttgcgcattcc ctctgtatcg tcttcgagag 1020
 69 ttctgcattc gtggggaaaaa gaagaattcc tcctccggaa tcagtgggtc ccagcggcgc 1080
 71 tacattgggg tggatgtatgc gaccctgagt cccagcatcc ttgctgaact acagttcga 1140
 73 gaacccaagct ttcccgatgt tcagcatggt gtactcatcc ataaagtcat cctgggctcc 1200
 75 cctgcacacc gggctgggtct gcggcctggt gatgtgattt tggccattgg ggagcagatg 1260
 77 gtacaaaatg ctgaagatgt ttatgaagct gttcgaaccc aatcccagtt ggcagtgcag 1320

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79 atccggcgaaac actgaccc ttatgtgaccc ctgaggcac agaatga 1377
 82 <210> SEQ ID NO: 2
 83 <211> LENGTH: 458
 84 <212> TYPE: PRT
 85 <213> ORGANISM: Homo sapiens
 87 <220> FEATURE:
 88 <221> NAME/KEY: misc_feature
 89 <223> OTHER INFORMATION: HtrA2 precursor protein
 92 <400> SEQUENCE: 2
 94 Met Ala Ala Pro Arg Ala Gly Arg Gly Ala Gly Trp Ser Leu Arg Ala
 95 1 5 10 15
 98 Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
 99 20 25 30
 102 Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
 103 35 40 45
 106 Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly
 107 50 55 60
 110 Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
 111 65 70 75 80
 114 Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
 115 85 90 95
 118 Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
 119 100 105 110
 122 Ala Gly Gly Ala Val Leu Leu Leu Trp Gly Gly Arg Gly Pro
 123 115 120 125
 126 Pro Ala Val Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg
 127 130 135 140
 130 Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
 131 145 150 155 160
 134 Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
 135 165 170 175
 138 Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu
 139 180 185 190
 142 Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Val Arg Val
 143 195 200 205
 146 Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
 147 210 215 220
 150 Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu
 151 225 230 235 240
 154 Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe
 155 245 250 255
 158 Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser
 159 260 265 270
 162 Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro
 163 275 280 285
 166 Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly
 167 290 295 300
 170 Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val
 171 305 310 315 320

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174 Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp
175 325 330 335
178 Arg Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser
179 340 345 350
182 Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr
183 355 360 365
186 Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe
187 370 375 380
190 Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser
191 385 390 395 400
194 Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile
195 405 410 415
198 Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg
199 420 425 430
202 Thr Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu
203 435 440 445
206 Thr Leu Tyr Val Thr Pro Glu Val Thr Glu
207 450 455
210 <210> SEQ ID NO: 3
211 <211> LENGTH: 981
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
215 <220> FEATURE:
216 <221> NAME/KEY: misc_feature
217 <223> OTHER INFORMATION: DNA that codes for mature HtrA2
220 <400> SEQUENCE: 3
221 atggccgtcc cttagcccgcc gccccgttct ccccgaggatc agtacaacctt catcgcatat 60
223 gtgggtggaga agacagcacc tgccgtggtc tataatcgaga tcctggacccg gcacccttcc 120
225 ttggggccgcg aggtccctat ctgcacacggc tcaggattcg tgggtggctgc cgatgggctc 180
227 attgtcacca acgcacatgt ggtggctgtat cggcgcagag tccgtgtgag actgctaagg 240
229 ggcgcacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcaacgctg 300
231 aggattcaga ctaaggagcc tctccccacg ctgcctctgg gacgctcagc tggatgtccgg 360
233 caagggggagt ttgttgttgc catggaaat ccctttgcac tgcagaacac gatcacatcc 420
235 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactccccca aaccaatgtg 480
237 gaatacattt aaactgtatgc agtattgtat tttggaaact ctggaggtcc cctggtaac 540
239 ctggatgggg aggtgattgg agtgaacacc atgaaggatca cagctggaaat ctcccttgcc 600
241 atcccttctg atcgtcttcg agagttctg catcgtgggg aaaagaagaa ttccctcctcc 660
243 ggaatcagtg ggtccacagcg gcgcctacatt ggggtgtatga tgctgaccct gagtcccagc 720
245 atcccttctg aactacagct tcgagaacca agcttcccg atgttcagca tgggtgtactc 780
247 atccataaaag tcatcctggg ctccccctgca caccgggctg gtctggggcc tgggtatgtg 840
249 attttggcca ttggggagca gatggtacaa aatgtgaag atgttatga agctgttcga 900
251 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgtg 960
253 accccctgagg tcacagaatg a 981
256 <210> SEQ ID NO: 4
257 <211> LENGTH: 326
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <221> NAME/KEY: misc_feature

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263 <223> OTHER INFORMATION: mature HtrA2
 266 <400> SEQUENCE: 4
 268 Met Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg Ser Gln Tyr Asn
 269 1 5 10 15
 272 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
 273 20 25 30
 276 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
 277 35 40 45
 280 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
 281 50 55 60
 284 Ala His Val Val Ala Asp Arg Arg Val Arg Val Arg Leu Leu Ser
 285 65 70 75 80
 288 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
 289 85 90 95
 292 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
 293 100 105 110
 296 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met
 297 115 120 125
 300 Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser Gly Ile Val Ser
 301 130 135 140
 304 Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro Gln Thr Asn Val
 305 145 150 155 160
 308 Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly Asn Ser Gly Gly
 309 165 170 175
 312 Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val Asn Thr Met Lys
 313 180 185 190
 316 Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp Arg Leu Arg Glu
 317 195 200 205
 320 Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser Gly Ile Ser Gly
 321 210 215 220
 324 Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr Leu Ser Pro Ser
 325 225 230 235 240
 328 Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe Pro Asp Val Gln
 329 245 250 255
 332 His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser Pro Ala His Arg
 333 260 265 270
 336 Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile Gly Glu Gln Met
 337 275 280 285
 340 Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg Thr Gln Ser Gln
 341 290 295 300
 344 Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu Thr Leu Tyr Val
 345 305 310 315 320
 348 Thr Pro Glu Val Thr Glu
 349 325
 352 <210> SEQ ID NO: 5
 353 <211> LENGTH: 981
 354 <212> TYPE: DNA
 355 <213> ORGANISM: Artificial
 357 <220> FEATURE:

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358 <223> OTHER INFORMATION: Polynucleotide consisting of the same base sequence of SEQ ID NO:

359 3 wherein the nucleotide of position 520 is g
361 <220> FEATURE:
362 <221> NAME/KEY: misc_feature
363 <223> OTHER INFORMATION: DNA that codes for mature HtrA2 (S306A)
366 <400> SEQUENCE: 5
367 atggccgtcc cttagccgccc gcccgccttc ccccgaggc agtacaactt catcgagat 60
369 gtgggtggaga agacagcacc tgccgtggtc tatacgaga tcctggaccg gcacccttc 120
371 ttggggccgcg aggtccctat ctcgaacggc tcaggattcg tgggtggctgc cgatgggctc 180
373 attgtcacca acgccccatgt ggtggctgtat cggcgcagag tccgtgtgag actgctaagc 240
375 ggcgcacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcacacgt 300
377 aggattcaga ctaaggagcc tctcccccacg ctgcctctgg gacgctcagc tggatgtccgg 360
379 caaggggaggt ttgttggc catggaaat cccttgcac tgcagaacac gatcacatcc 420
381 ggcattgtta gctctgctca ggcgtccagcc agagacctgg gactccccca aaccaatgtg 480
383 gaatacattc aaactgtatgc agtattgtat tttggaaacg ctggagggtcc cctgggttaac 540
385 ctggatgggg aggtgattgg agtgaacacc atgaaggatca cagctggaaat ctcccttgc 600
387 atcccttctg atcgtcttcg agagtttctg catcggtggg aaaagaagaa ttcccttgc 660
389 ggaatcgtg ggtcccaagcg ggcgtacatt ggggtgatga tgctgaccct gagtcccagc 720
391 atccctgctg aactacagct tcgagaacca agcttcccg atgttcagca tggatgtactc 780
393 atccataaaag tcatcctggg ctccctgcg caccgggctg gtctgcggcc tggatgtg 840
395 attttggcca ttggggagca gatggtacaa aatgctgaag atgttatga agctgttgc 900
397 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgt 960
399 accccctgagg tcacagaatg a 981
402 <210> SEQ ID NO: 6
403 <211> LENGTH: 326
404 <212> TYPE: PRT
405 <213> ORGANISM: Artificial
407 <220> FEATURE:
408 <223> OTHER INFORMATION: Polypeptide consisting of the same amino acid sequence of SEQ ID NO:

409 NO:4 wherein the 174th amino acid residue is substituted by Ala
411 <220> FEATURE:
412 <221> NAME/KEY: misc_feature
413 <223> OTHER INFORMATION: mature HtrA2 (S306A)
416 <400> SEQUENCE: 6
418 Met Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg Ser Gln Tyr Asn
419 1 5 10 15
422 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
423 20 25 30
426 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
427 35 40 45
430 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
431 50 55 60
434 Ala His Val Val Ala Asp Arg Arg Val Arg Val Arg Leu Leu Ser
435 65 70 75 80
438 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
439 85 90 95
442 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
443 100 105 110
446 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/13/2006
PATENT APPLICATION: US/10/563,073 TIME: 10:27:41

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\01132006\J563073.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date